## Amendments to the Claims:

This listing of claims will replace all prior versions, and listings, of claims in the application:

## Listing of Claims:

1 (currently amended). A method of fitting a plurality of sub-population functions to digital image data, comprising the steps of:

defining <u>a plurality of collections, each of said collections having</u> a plurality of functions according to a plurality of function parameters and a total number of functions;

~~generating a model based on said plurality of function parameters;~~

determining an objective function for the fitting error between <u>each</u> <u>of</u> said ~~model~~ <u>collections</u> and the data;

comparing <u>each</u> said fitting error to stopping criteria to determine if said stopping criteria is satisfied; ~~and~~

if, at said comparing step, ~~said fitting error does not satisfy~~ said stopping criteria is not satisfied, then altering said plurality of function parameters and said total number of functions in randomly selected said collections, and

following said altering step, repeating said ~~generating,~~ determining, ~~and~~ comparing, and altering steps ~~if, at said comparing step, said fitting error does not satisfy said stopping criteria~~.

2 (currently amended). The method of Claim 1 wherein said ~~model is~~ <u>collections are each</u> defined as a vector representation of said plurality of function parameters.

3 (currently amended). The method of Claim 1 further comprising the steps of specifying at least a first threshold value delineating said plurality of functions <u>of each of said collections</u>.

4 (original). The method of Claim 3 wherein said at least a first threshold value is calculated based upon the likelihood of misclassification of data.

5 (original).  The method of Claim 3 further comprising the step of segmenting the data according to said at least a first threshold value.

6 (currently amended).  The method of Claim ~~1~~ 3 wherein said ~~objective function is~~ collections are each defined as a vector representation of said plurality of function parameters.

7 (currently amended)..  The method of Claim 2 wherein said altering step is accomplished by evolving said plurality of ~~function parameters and said total number of functions~~ collections according to a genetic algorithm.

8 (currently amended).  The method of Claim 7 wherein said ~~genetic algorithm evolves said plurality of function parameters through mutation and crossover~~ evolving includes crossover followed by mutation.

9 (original).  The method of Claim 1 wherein said plurality of functions are normal distributions, and said plurality of functions parameters include the mean and standard deviations of said normal distributions.

10 (original).  The method of Claim 1 wherein said comparing step includes the utilization of a statistical f-test to evaluate the relative contribution of each of said plurality of functions in comparison of said fitting error and the data.

11 (original).  The method of Claim 1 wherein the data is organized as a histogram.

12 (original).  The method of Claim 1 wherein said stopping criteria are defined by a fitness function.

13 (currently amended).  The method of Claim 12 wherein said fitness function is optimized to minimize the magnitude of the fit error between ~~said model~~ each of said collections and the data.

14 (currently amended). An apparatus for fitting a plurality of sub-population functions to digital image data, comprising:

means for defining a plurality of collections, each of said collections having a plurality of functions according to a plurality of function parameters and a total number of functions;

~~means for generating an objective function based on said plurality of function parameters;~~

means for determining a fitting error between ~~said objective function~~ each of said collections and the data;

means for comparing each said fitting error to stopping criteria to determine if said stopping criteria is satisfied; and

means for altering said plurality of function parameters and said total number of functions randomly in one or more of said collections, if said means for comparing determines that said fitting error is not satisfied~~, said apparatus operable to said generating, determining, and comparing operations~~.

15 (currently amended). The apparatus of Claim 14 wherein said ~~model is~~ collections are each defined as a vector representation of said plurality of function parameters.

16 (original). The apparatus of Claim 14 further comprising means for specifying at least a first threshold value delineating said plurality of functions.

17 (original). The apparatus of Claim 16 wherein said at least a first threshold value is calculated based upon the likelihood of misclassification of data.

18 (original). The apparatus of Claim 16 further comprising means for segmenting the data according to said at least a first threshold value.

19 (cancelled).

20 (currently amended). The apparatus of Claim 15 wherein said means for altering operation is accomplished by evolving said plurality of ~~function parameters and said total number of functions~~ collections according to a genetic algorithm.

21 (currently amended). The apparatus of Claim 20 wherein said genetic algorithm ~~evolves said plurality of function parameters through mutation and crossover~~ includes crossover followed by mutation.

22 (original). The apparatus of Claim 14 wherein said plurality of functions are normal distributions, and said plurality of functions parameters include the mean and standard deviations of said normal distributions.

23 (original). The apparatus of Claim 14 wherein said means for comparing includes the utilization of a statistical f-test to evaluate the relative contribution of each of said plurality of functions in comparison of said fitting error and the data.

24 (original). The apparatus of Claim 14 wherein the data is organized as a histogram.

25 (original). The apparatus of Claim 14 wherein said stopping criteria are defined by a fitness function.

26 (currently amended). The apparatus of Claim 25 wherein said fitness function is optimized to minimize the magnitude of the fit error between said ~~objective function~~ each of said collections and the data.

Claims 27-44 (cancelled).

45 (currently amended). A method of specifying thresholds for segmenting a digital image, comprising the steps of:
producing a histogram of the image, the histogram having histogram data;

defining a <u>collection of mixture models, each said</u> mixture model ~~as~~ <u>being</u> a combination of a plurality of subpopulations; wherein each subpopulation is a function defined according to a plurality of function parameters;

defining a <u>generation of chromosomes, each said</u> chromosome ~~to be~~ <u>being</u> a vector encoding <u>a respective one</u> of the mixture ~~model~~ <u>models</u> wherein the elements of the vector encode the <u>respective</u> plurality of function parameters of the plurality of subpopulations;

~~forming a generation; wherein a generation comprises a plurality of chromosomes and a master chromosome;~~

for each chromosome in the generation, performing the following steps:

determining the fitting error between the mixture model defined by the chromosome and the histogram data;

determining a measure of the relative contributions of the individual sub-populations defined by the chromosome; and

determining a fitness value based on said fitting error and said measure of relative contributions;

comparing said fitness values to stopping criteria;

altering said <u>plurality of function parameters and said total number of functions in randomly selected</u> chromosomes <u>of said generation to define a next generation of chromosomes, if none of said fitness values satisfies said stopping criteria;</u> and

repeating said ~~producing, first and second defining, and forming~~ <u>performing, comparing, and altering</u> steps <u>on said next generation of chromosomes,</u> if none of said fitness values satisfies said stopping criteria; and

specifying at least a first threshold value delineating said subpopulations in ~~the~~ <u>a respective said</u> mixture model, if at least one of said fitness values satisfies said stopping criteria.

46 (previously submitted). The method of Claim 45 wherein said at least a first threshold value is calculated based upon the likelihood of misclassification of said histogram data.

47 (cancelled).

48 (currently amended). The method of Claim 45 wherein said altering step is accomplished by evolving said ~~plurality of function parameters and said total number of functions~~ chromosomes according to a genetic algorithm.

49 (currently amended). The method of Claim 48 wherein said ~~genetic algorithm evolves said plurality of function parameters through mutation and crossover~~ evolving includes crossover followed by mutation.

50 (previously submitted). The method of Claim 45 wherein said plurality of functions are normal distributions, and said plurality of functions parameters include the mean and standard deviations of said normal distributions.

51 (previously submitted). The method of Claim 45 wherein said comparing step includes the utilization of a statistical f-test to evaluate the relative contribution of each of said plurality of functions in comparison of said fitting error and the data.

52 (previously submitted). The method of Claim 45 wherein said stopping criteria are defined by a fitness function.

53 (currently amended). The method of Claim 52 wherein said fitness function is optimized to minimize the magnitude of the fit error between said ~~objective function~~ mixture model and the data.

54 (currently amended). An apparatus for specifying thresholds for segmenting a digital image, comprising the steps of:
means for producing a histogram of the image, the histogram having histogram data;
means for defining a collection of mixture models, each said mixture model ~~as~~ being a combination of a plurality of subpopulations; wherein each subpopulation is a function defined according to a plurality of function parameters;

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means for defining a <u>generation of chromosomes, each said</u> chromosome ~~to be~~ <u>being</u> a vector encoding <u>a respective one</u> of the mixture ~~model~~ <u>models</u> wherein the elements of the vector encode the <u>respective</u> plurality of function parameters of the plurality of subpopulations;

~~means for forming a generation; wherein a generation comprises a plurality of chromosomes and a master chromosome;~~

for each chromosome in the generation, means for performing the following steps:

determining the fitting error between the mixture model defined by the chromosome and the histogram data;

determining a measure of the relative contributions of the individual sub-populations defined by the chromosome; and

determining a fitness value based on said fitting error and said measure of relative contributions;

means for comparing said fitness values to stopping criteria;

means for altering said <u>plurality of function parameters and said total number of functions in randomly selected</u> chromosomes <u>of said generation to define a next generation of chromosomes, if none of said fitness values satisfies said stopping criteria;</u> and

repeating said ~~producing, first and second defining, and forming~~ <u>performing, comparing, and</u> altering steps <u>on said next generation of chromosomes</u>, if none of said fitness values satisfies said stopping criteria; and

means for specifying at least a first threshold value delineating said sub-populations in ~~the~~ <u>a respective said</u> mixture model, if at least one of said fitness values satisfies said stopping criteria.